

0/506630

SEQUENCE LISTING

<110> GOKHALE, Rajesh
TSUJI, Stuart
KHOSLA, Chaitan
WU, Nicholas
CANE, David

<120> METHODS TO MEDIATE POLYKETIDE SYNTHASE
MODULE EFFECTIVENESS

<130> 300622004601

<140> US 10/506,630

<141> 2002-03-04

<150> PCT/US03/06910

<151> 2002-03-04

<150> US 10/091,244

<151> 2002-03-04

<150> 60/361,758

<151> 2002-03-04

<160> 41

<170> FastSEQ for Windows Version 4.0

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<223> Nhe site upstream of the KS at position 7570

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<223> Nhe site upstream of the KS at position 28710

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gctagcgacc cgatc

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<210> 3

<211> 31

<212> PRT

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<223> N-terminal linker of M3

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 Asp Leu Arg Ala Ala Arg Gln Arg Ile Arg Glu Leu Glu Ser Asp
 20 25 30

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<400> 5
 gggaattcag gtcctctccc ccgc 24

<210> 6
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<220>
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 gaattcctac aggtcctctc cccc 24

<210> 8
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<400> 8
ccatatgctg cgcgaccggc tg

22

<210> 9
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<220>
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<400> 9
gaattctcaa tcgccgtcga gctcc

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<210> 10
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<400> 10
ccatatggtg gtcgaccggc tcg

23

<210> 11
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<400> 11
actagtgagg aaaccggcga ccg

23

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ccatatgctg cgcgaccggc tg

22

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gaattcttag ccgagctc cgtc

24

<210> 14
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<400> 14
ccatatggtg gtcgaccggc tcg

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<210> 15
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<220>
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<400> 15
gaattcttag aacagcctgt cccgcag

27

<210> 16
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<220>
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<400> 16
ctgctcgaga ggctgttcgc ggcctca

27

<210> 17
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<220>
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<400> 17
cccgctgagc ctacaggtcc tctcccc

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<210> 18
<211> 18
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<220>
<223> Intra-polypeptide linker

<400> 18
Gly Gly Ala Thr Gly Ala Glu Gln Ala Ala Pro Ala Thr Thr Ala Pro
1 5 10 15

Val Asp

<210> 19
<211> 18
<212> PRT
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<220>
<223> Intra-polypeptide linker

<400> 19
Val Gly Asp Ala Asp Gln Ala Ala Val Arg Val Val Gly Ala Ala Asp
1 5 10 15
Glu Ser

<210> 20
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 20
Val Gly Ala Ala Glu Ala Glu Gln Ala Pro Ala Leu Val Arg Glu Val
1 5 10 15
Pro Lys Asp Ala Asp
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<210> 21
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 21
Phe Gly Ser Ala Ala Asn Arg Pro Ala Glu Ile Gly Thr Ala Ala Ala
1 5 10 15
Glu

<210> 22
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 22
Leu Gly Glu Arg Pro Ala Ala Pro Ala Pro Val Thr Arg Asp Val Ser
1 5 10 15
Asp

<210> 23
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 23
Gly Glu Thr Val Ala Gly Ala Pro Ala Thr Pro Val Thr Thr Val Ala
1 5 10 15
Asp Ala Gly

<210> 24
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 24
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Ala Val Gly Gln Asp
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<210> 25
<211> 21
<212> PRT
<213> Artificial Sequence

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<400> 25
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Val Val Gly Gln Asp
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<210> 26
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Intra-polypeptide linker

<400> 26
Glu Leu Phe Thr Gly Glu Asn Pro Ala Pro Val Arg Gly Pro Val Ser
1 5 10 15
Ala Gly Gln Asp
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<210> 27

<211> 30
<212> PRT
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<220>
<223> N-Terminal Inter-polypeptide linker

<400> 27
Val Thr Asp Ser Glu Lys Val Ala Glu Tyr Leu Arg Arg Ala Thr Leu
1 5 10 15
Asp Leu Arg Ala Ala Arg Gln Arg Ile Arg Glu Leu Glu Ser
20 25 30

<210> 28
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 28
Met Ser Gly Asp Asn Gly Met Thr Glu Glu Lys Leu Arg Arg Tyr Leu
1 5 10 15
Lys Arg Thr Val Thr Glu Leu Asp Ser Val Thr Ala Arg Leu Arg Glu
20 25 30
Val Glu His Arg Ala Gly
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<210> 29
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 29
Met Ser Ala Pro Asn Glu Gln Ile Val Asp Ala Leu Arg Ala Ser Leu
1 5 10 15
Lys Glu Asn Val Arg Leu Gln Gln Glu Asn Ser Ala Leu Ala Ala Ala
20 25 30
Ala Ala

<210> 30
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 30
Val Ser Ala Ser Tyr Glu Lys Val Val Glu Ala Leu Arg Lys Ser Leu
1 5 10 15
Glu Glu Val Gly Thr Leu Lys Lys Arg Asn Arg Gln Leu Ala Asp Ala
20 25 30
Ala Gly

<210> 31
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 31
Val Ala Asp Glu Gly Gln Leu Arg Asp Tyr Leu Lys Arg Ala Ile Ala
1 5 10 15
Asp Ala Arg Asp Ala Arg Thr Arg Leu Arg Glu Val Glu Glu Gln Ala
20 25 30
Arg

<210> 32
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 32
Met Ala Thr Asp Glu Lys Leu Leu Lys Tyr Leu Lys Arg Val Thr Ala
1 5 10 15
Glu Leu His Ser Leu Arg Lys Gln Gly Ala Arg His Ala Asp
20 25 30

<210> 33
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 33
Met Arg Glu Asp Gln Leu Leu Asp Ala Leu Arg Lys Ser Val Lys Glu
1 5 10 15
Asn Ala Arg Leu Arg Lys Ala Asn Thr Ser Leu Arg Ala Ala Met Asp
20 25 30

<210> 34
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> N-Terminal Inter-polypeptide linker

<400> 34
Met Pro Glu Gln Asp Lys Val Val Glu Tyr Leu Arg Trp Ala Thr Ala
1 5 10 15
Glu Leu His Thr Thr Arg Ala Lys Leu Glu Ala Leu Ala Ala Ala Asn

Thr

20

25

30

<210> 35
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<212> PRT
<213> Artificial Sequence

<220>
<223> Alignment of the EryA SU

<400> 35
Val Val Phe Val Phe Pro Gly Gln Gly Ala Gln Trp Ala Gly Met Ala
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Gly Glu Leu Ile Gly Glu Ser Arg Val Phe Ala Ala Met Asp Ala
20 25 30
Cys Ala Arg Ala Phe Glu Pro Val Thr Asp Trp Thr Leu Ala Gln Val
35 40 45
Leu Asp Ser Pro Glu Gln Ser Arg Arg Val Glu Val Val Gln Pro Ala
50 55 60
Leu Phe Ala Val Gln Thr Ser Leu Ala Ala Leu Trp Arg Ser Phe Gly
65 70 75 80
Val Thr Pro Asp Ala Val Val Gly His Ser Ile Gly Glu Leu Ala Ala
85 90 95
Ala His Val Cys Gly Ala Ala Gly Ala Ala Asp Ala Ala Arg Ala Ala
100 105 110
Ala Leu Trp Ser Arg Glu Met Ile Pro Ile Val Gly Asn Gly Asp Met
115 120 125
Met Ala Val Ala Leu Ser Ala Asp Glu Ile Glu Pro Arg Ile Ala Arg
130 135 140
Trp Asp Asp Val Val Leu Ala Gly Val Asn Gly Pro Arg Ser Val Leu
145 150 155 160
Leu Thr Gly Ser Pro Glu Pro Val Ala Arg Arg Val Gln Glu Leu Ser
165 170 175
Ala Glu Gly Val Arg Ala Gln Val Ile Asn Val Ser Met Ala Ala His
180 185 190
Ser Ala Gln Val Asp Asp Ile Ala Glu Gly Met Arg Ser Ala Leu Ala
195 200 205
Trp Phe Ala Pro Gly Gly Ser Glu Val Pro Phe Tyr Ala Ser Leu Thr
210 215 220
Gly Gly Ala Val Asp Thr Arg Glu Leu Val Ala Asp Tyr Trp Arg Arg
225 230 235 240
Ser Phe Arg Leu Pro Val Arg Phe Asp Glu Ala Ile Arg Ser Ala Leu
245 250 255
Glu Val Gly Pro Gly Thr Phe Val Glu Ala Ser Pro His Pro Val Ile
260 265 270
Ala Ala Ala Leu Gln Gln Thr Leu Asp Ala Glu Gly Ser Ser Ala Ala
275 280 285
Val Val Pro Thr Leu Gln Arg Gly Gln Gly Gly Met Arg Arg Phe Leu
290 295 300
Leu Ala Ala Ala Gln Ala Phe Thr Gly Gly Val Ala Val Asp Trp Thr
305 310 315 320
Ala Ala Tyr Asp Asp Val Gly Pro Asn Pro Ala Leu Gly Arg Glu Ala
325 330 335
Asp Ala Glu Ala Thr Phe Arg Glu Leu Gly Leu Asp Ser Val Leu Ala
340 345 350
Ala Gln Ile Arg Ala Lys Val Ser Ala Ala Ile Gly Arg Glu Val Asn
355 360 365
Ile Ala Leu Leu Tyr Asp His Pro Thr Pro Arg Ala Leu Ala Glu Ala
370 375 380
Leu Ala Ala Gly

<210> 36
 <211> 1397
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Alignment of the EryA SU

<400> 36
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 Pro Gly Gly Val Ser Thr Pro Glu Glu Phe Trp Glu Leu Leu Ser Glu
 20 25 30
 Gly Arg Asp Ala Val Ala Gly Leu Pro Thr Asp Arg Gly Trp Asp Leu
 35 40 45
 Asp Ser Leu Phe His Pro Asp Pro Thr Arg Ser Gly Thr Ala His Gln
 50 55 60
 Arg Gly Gly Gly Phe Leu Thr Glu Ala Thr Ala Phe Asp Pro Ala Phe
 65 70 75 80
 Phe Gly Met Ser Pro Arg Glu Ala Leu Ala Val Asp Pro Gln Gln Arg
 85 90 95
 Leu Met Leu Glu Leu Ser Trp Glu Val Leu Glu Arg Ala Gly Ile Pro
 100 105 110
 Pro Thr Ser Ile Gln Ala Ser Pro Thr Gly Val Phe Val Gly Leu Ile
 115 120 125
 Pro Gln Glu Tyr Gly Pro Arg Leu Ala Glu Gly Gly Glu Gly Val Glu
 130 135 140
 Gly Tyr Leu Met Thr Gly Thr Thr Thr Ser Val Ala Ser Gly Arg Ile
 145 150 155 160
 Ala Tyr Thr Leu Gly Leu Glu Gly Pro Ala Ile Ser Val Asp Thr Ala
 165 170 175
 Cys Ser Ser Ser Leu Val Ala Val His Leu Ala Cys Gln Ser Leu Arg
 180 185 190
 Arg Gly Glu Ser Ser Ile Ala Met Ala Gly Gly Val Thr Val Met Pro
 195 200 205
 Thr Pro Gly Met Leu Val Asp Phe Ser Arg Met Asn Ser Leu Ala Pro
 210 215 220
 Asp Gly Arg Cys Lys Ala Phe Ser Ala Gly Ala Asn Gly Phe Gly Met
 225 230 235 240
 Ala Glu Gly Ala Gly Met Leu Leu Ile Glu Arg Leu Ser Asp Ala Arg
 245 250 255
 Arg Asn Gly His Pro Val Leu Ala Val Leu Arg Gly Thr Ala Val Asn
 260 265 270
 Ser Asp Gly Ala Ser Asn Gly Leu Ser Ala Pro Asn Gly Arg Ala Gln
 275 280 285
 Val Arg Val Ile Gln Gln Ala Leu Ala Glu Ser Gly Leu Gly Pro Ala
 290 295 300
 Asp Ile Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp
 305 310 315 320
 Pro Ile Glu Ala Arg Ala Leu Phe Glu Ala Tyr Gly Arg Asp Arg Glu
 325 330 335
 Gln Pro Leu His Leu Gly Ser Val Lys Ser Asn Leu Gly His Thr Gln
 340 345 350
 Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg
 355 360 365
 Ala Gly Thr Leu Pro Arg Thr Leu His Ala Ser Glu Arg Ser Lys Glu
 370 375 380
 Ile Asp Trp Ser Ser Gly Ala Ile Ser Leu Ile Asp Glu Pro Glu Pro
 385 390 395 400

Trp	Pro	Ala	Gly	Ala	Arg	Pro	Arg	Arg	Ala	Gly	Val	Ser	Ser	Phe	Gly
				405					410					415	
Ile	Ser	Gly	Thr	Asn	Ala	His	Ala	Ile	Ile	Glu	Glu	Ala	Pro	Gln	Val
				420				425					430		
Val	Glu	Gly	Glu	Arg	Val	Glu	Ala	Gly	Asp	Val	Val	Ala	Pro	Trp	Val
		435					440					445			
Leu	Ser	Ala	Ser	Ser	Ala	Glu	Gly	Leu	Arg	Ala	Gln	Ala	Ala	Arg	Leu
	450					455					460				
Ala	Ala	His	Leu	Arg	Glu	His	Pro	Gly	Gln	Asp	Pro	Arg	Asp	Ile	Ala
465					470					475					480
Tyr	Ser	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Leu	Pro	His	Arg	Ala	Ala	Phe
				485					490					495	
Ala	Pro	Val	Asp	Glu	Ser	Ala	Ala	Leu	Arg	Val	Leu	Asp	Gly	Leu	Ala
			500					505					510		
Thr	Gly	Asn	Ala	Asp	Gly	Ala	Ala	Val	Gly	Thr	Ser	Arg	Ala	Gln	Gln
		515					520					525			
Arg	Ala	Val	Phe	Val	Trp	Ala	Ala	Val	Asp	Asp	Thr	Ser	Pro	Ala	Ala
	530					535					540				
Leu	Arg	Glu	Ala	Asp	Ala	Leu	Glu	Pro	His	Leu	Asp	Arg	Glu	Val	Ile
545					550					555					560
Pro	Phe	Leu	Arg	Ala	Glu	Ala	Ala	Arg	Arg	Glu	Gln	Asp	Ala	Ala	Leu
				565					570					575	
Ser	Thr	Glu	Asp	Val	Val	Met	Ala	Val	Met	Val	Ser	Met	Arg	Ala	His
			580					585					590		
Val	Glu	Ala	Ile	Gln	Ile	Cys	Ala	Ala	Leu	Ser	Leu	Asp	Asp	Ala	Ala
		595					600					605			
Arg	Val	Val	Ala	Leu	Arg	Ser	Arg	Val	Ile	Ala	Thr	Met	Pro	Gly	Asn
	610					615					620				
Lys	Gly	Ala	Ser	Ile	Ala	Ala	Pro	Ala	Gly	Glu	Val	Arg	Ala	Arg	Ile
625					630					635					640
Gly	Asp	Arg	Val	Glu	Ile	Ala	Gly	Arg	Ser	Val	Val	Val	Ala	Asp	Ser
				645					650					655	
Asp	Glu	Leu	Asp	Arg	Leu	Val	Ala	Ser	Cys	Thr	Thr	Glu	Cys	Ile	Arg
			660					665					670		
Ala	Lys	Arg	Leu	Ala	Asp	Tyr	Ser	Ser	Ser	His	Val	Glu	Thr	Ile	Arg
		675					680					685			
Asp	Ala	Leu	His	Ala	Glu	Leu	Gly	Glu	Asp	Phe	His	Pro	Leu	Pro	Gly
	690					695				700					
Phe	Val	Pro	Phe	Phe	Thr	Val	Thr	Gly	Arg	Trp	Thr	Gln	Pro	Asp	Glu
705					710					715					720
Leu	Asp	Ala	Gly	Tyr	Arg	Asn	Ile	Arg	Thr	Arg	Ala	Asp	Val	Arg	Ala
				725					730					735	
Leu	Ala	Glu	Gln	Tyr	Arg	Thr	Leu	Val	Ala	Ile	Leu	Thr	Ala	Ala	Ile
			740					745					750		
Glu	Glu	Ile	Gly	Asp	Gly	Ser	Gly	Ala	Asp	Leu	Ser	Ala	Ile	His	Ser
		755					760					765			
Arg	Gly	Asp	Gly	Ser	Leu	Ala	Asp	Phe	Gly	Glu	Ala	Leu	Ser	Arg	Phe
	770					775					780				
Ala	Ala	Ala	Val	Asp	Trp	Glu	Ser	Val	His	Leu	Gly	Thr	Gly	Ala	Arg
785					790					795					800
Arg	Val	Pro	Leu	Pro	Thr	Tyr	Pro	Phe	Gln	Arg	Glu	Arg	Val	Trp	Leu
				805					810					815	
Glu	Pro	Lys	Pro	Val	Ala	Arg	Arg	Ser	Thr	Glu	Val	Asp	Glu	Val	Ser
			820					825					830		
Ala	Leu	Arg	Tyr	Arg	Ile	Glu	Trp	Arg	Pro	Thr	Gly	Ala	Gly	Glu	Pro
		835					840					845			
Ala	Arg	Leu	Asp	Gly	Thr	Trp	Leu	Val	Ala	Lys	Tyr	Ala	Gly	Thr	Ala
	850					855					860				
Asp	Glu	Thr	Ser	Thr	Ala	Ala	Arg	Glu	Ala	Leu	Glu	Ser	Ala	Gly	Ala
865					870					875					880
Arg	Val	Arg	Glu	Leu	Val	Val	Asp	Ala	Arg	Cys	Gly	Arg	Asp	Glu	Leu
				885					890					895	

Ala Glu Arg Leu Arg Ser Val Gly Glu Val Ala Gly Val Leu Ser Leu
 900 905 910
 Leu Ala Val Asp Glu Ala Glu Pro Glu Glu Ala Pro Leu Ala Leu Ala
 915 920 925
 Ser Leu Ala Asp Thr Leu Ser Leu Val Gln Ala Met Val Ser Ala Glu
 930 935 940
 Leu Gly Cys Pro Leu Trp Thr Val Thr Glu Ser Ala Val Ala Thr Gly
 945 950 955 960
 Pro Phe Glu Arg Val Arg Asn Ala Ala His Gly Ala Leu Trp Gly Val
 965 970 975
 Gly Arg Val Ile Ala Leu Glu Asn Pro Ala Val Trp Gly Gly Leu Val
 980 985 990
 Asp Val Pro Ala Gly Ser Val Ala Glu Leu Ala Arg His Leu Ala Ala
 995 1000 1005
 Val Val Ser Gly Gly Ala Gly Glu Asp Gln Leu Ala Leu Arg Ala Asp
 1010 1015 1020
 Gly Val Tyr Gly Arg Arg Trp Val Arg Ala Ala Pro Ala Thr Asp
 1025 1030 1035 1040
 Asp Glu Trp Lys Pro Thr Gly Thr Val Leu Val Thr Gly Gly Thr Gly
 1045 1050 1055
 Gly Val Gly Gly Gln Ile Ala Arg Trp Ile Ala Arg Pro Gly Ala Pro
 1060 1065 1070
 His Leu Leu Leu Val Ser Arg Ser Gly Pro Asp Ala Asp Gly Ala Gly
 1075 1080 1085
 Glu Leu Val Ala Glu Leu Glu Ala Leu Gly Ala Arg Thr Thr Val Ala
 1090 1095 1100
 Ala Cys Asp Val Ile Asp Arg Glu Ser Val Arg Glu Leu Leu Gly Gly
 1105 1110 1115 1120
 Ile Gly Asp Asp Val Pro Leu Ser Ala Val Phe His Ala Ala Ala Thr
 1125 1130 1135
 Leu Asp Asp Gly Thr Val Asp Thr Leu Thr Gly Glu Arg Ile Glu Arg
 1140 1145 1150
 Ala Ser Arg Ala Lys Val Leu Gly Ala Arg Asn Leu His Glu Leu Thr
 1155 1160 1165
 Arg Glu Leu Asp Leu Thr Ala His Val Leu Phe Ser Ser Phe Ala Ser
 1170 1175 1180
 Ala Phe Gly Ala Pro Gly Leu Gly Gly Tyr Ala Pro Gly Asn Ala Tyr
 1185 1190 1195 1200
 Leu Asp Gly Leu Ala Gln Gln Arg Arg Ser Asp Gly Leu Pro Ala Thr
 1205 1210 1215
 Ala Val Ala Trp Gly Thr Trp Ala Gly Ser Gly Met Ala Glu Gly Ala
 1220 1225 1230
 Val Ala Asp Arg Phe Arg Arg His Gly Val Ile Glu Met Pro Pro Glu
 1235 1240 1245
 Thr Ala Cys Arg Ala Leu Gln Asn Ala Leu Asp Arg Ala Glu Val Cys
 1250 1255 1260
 Pro Ile Val Ile Asp Val Arg Trp Asp Arg Phe Leu Leu Ala Tyr Thr
 1265 1270 1275 1280
 Ala Gln Arg Pro Thr Arg Leu Phe Asp Glu Ile Asp Asp Ala Arg Arg
 1285 1290 1295
 Ala Ala Pro Gln Ala Pro Ala Glu Pro Arg Val Gly Ala Leu Ala Ser
 1300 1305 1310
 Leu Pro Ala Pro Glu Arg Glu Glu Ala Leu Phe Glu Leu Val Arg Ser
 1315 1320 1325
 His Ala Ala Ala Val Leu Gly His Ala Ser Ala Glu Arg Val Pro Ala
 1330 1335 1340
 Asp Gln Ala Ala Glu Val Leu Ser Leu Glu Asn Arg Leu Gly Ala Ala
 1345 1350 1355 1360
 Thr Val Arg Leu Pro Thr Thr Thr Val Phe Asp Asp Val Arg Thr Leu
 1365 1370 1375
 Ala His Leu Ala Ala Glu Leu Gly Gly Ala Thr Gly Ala Glu Gln Ala
 1380 1385 1390

Ala Pro Ala Thr Thr
1395

<210> 37
<211> 1114
<212> PRT
<213> Artificial Sequence

<220>
<223> Alignment of the EryA SU

<400> 37
Ala Pro Val Asp Glu Ile Ile Gly Met Ala Leu Glu Val Asp Ser Glu
1 5 10 15
Arg Leu Glu Leu Ile Thr Ser Gly Arg Asp Ser Ala Ala Glu Val Asp
20 25 30
Val Pro Asp Glu Leu Met Ala Ser Asp Ala Ala Gly Thr Arg Ala His
35 40 45
Asn Phe Met Ala Gly Gly Asp Ala Ala Ile Ser Leu Met Gln Ala Thr
50 55 60
Thr Ala Leu Ser Ile Pro Glu Thr Arg Gly Ser Asp Val Met Ser His
65 70 75 80
Gln Gly Ala Thr Gly Arg Pro Arg Pro Glu Asp Gly Val Asp Leu Leu
85 90 95
Thr Asn Thr Ala Ser Ala Ile Ala Val Leu Leu Ala Leu Thr Ser Val
100 105 110
Ala Leu Thr Cys Gly Ser Asp Gly Asp Gln Gly Leu Val Ala Val Ser
115 120 125
Ala Gly Glu Val Phe Thr Glu Ser Arg Gln Gly Ala Ser Pro Cys Pro
130 135 140
Ser Asp Glu Asp Gly Leu Gly Ser Ala Phe Val Val Gln Arg Asp Arg
145 150 155 160
Glu Arg Arg Gly Val Val Ala Ser Val Gln Ser Ser Val Ala Gln Arg
165 170 175
Arg Trp Ala Arg Ala Ile Thr Gly Ala Val Ala Val Arg Val Ala Ser
180 185 190
Leu Ala Thr Lys Ser Gly Ser Ser Gly Val Leu Leu Ser Ile Ala Val
195 200 205
Ala Ile Val Ile Gly Leu Glu Arg Val Val Pro Met Cys Arg Gly Arg
210 215 220
Ser Gly Leu Ile Asp Ser Ser Glu Ile Glu Leu Ala Asp Gly Val Arg
225 230 235 240
Glu Ser Pro Ala Ala Asp Gly Val Gly Ala Val Val Ile Ala Pro Glu
245 250 255
Pro Glu Pro Val Pro Gln Pro Arg Arg Met Leu Pro Ala Thr Gly Val
260 265 270
Val Val Val Leu Ala Arg Thr Gly Ala Ala Leu Arg Gly Arg Leu Ala
275 280 285
Asp His Leu Ala Ala His Pro Gly Ile Ala Pro Ala Asp Val Ser Trp
290 295 300
Thr Met Arg Ala Gln His Phe Glu Glu Ala Val Leu Ala Ala Asp Thr
305 310 315 320
Ala Glu Ala Val His Arg Arg Ala Val Asp Ala Val Val Pro Gly Val
325 330 335
Val Thr Gly Ser Ala Ser Asp Gly Gly Ser Val Phe Val Ala Glu Ala
340 345 350
Arg Glu Pro Val Pro Glu Ser Ile Ala Glu Asp Ala Val Leu Ser Glu
355 360 365
Val Ala Gly Arg Ser Val Ser Glu Val Leu Glu Pro Arg Pro Asp Ala
370 375 380
Pro Ser Leu Glu Asp Val Val Leu Ala Val Met Val Arg Leu Arg Ala

385					390					395				400
Cys	Ala	Val	Ser	Ile	Gln	Ile	Val	Ala	Ala	Leu	Ser	Leu	Glu	Asp
				405					410					415
Met	Arg	Val	Val	Ala	Arg	Arg	Ser	Arg	Ala	Val	Arg	Ala	Val	Ala
			420					425					430	
Arg	Gly	Ser	Leu	Ser	Val	Arg	Gly	Gly	Arg	Ser	Asp	Val	Glu	Lys
		435					440					445		
Leu	Ala	Asp	Asp	Ser	Trp	Thr	Gly	Arg	Leu	Glu	Val	Ala	Gly	Asp
	450					455					460			
Val	Val	Val	Ala	Asp	Ala	Gln	Ala	Ala	Arg	Glu	Phe	Leu	Glu	Tyr
465					470					475				480
Glu	Gly	Val	Gly	Ile	Arg	Ala	Arg	Ala	Ile	Pro	Asp	Tyr	Ser	Thr
				485					490					495
His	Val	Glu	Pro	Val	Arg	Asp	Glu	Leu	Val	Gln	Ala	Leu	Ala	Gly
			500					505					510	
Thr	Pro	Arg	Arg	Ala	Glu	Val	Pro	Phe	Phe	Thr	Leu	Thr	Gly	Asp
		515					520					525		
Leu	Asp	Gly	Thr	Glu	Leu	Asp	Ala	Gly	Tyr	Arg	Asn	Ile	His	Pro
	530					535					540			
His	Ser	Val	Gln	Ala	Leu	Thr	Asp	Gln	Tyr	Ala	Thr	Ile	Val	Pro
545					550					555				560
Leu	Ala	Ser	Ser	Val	Gln	Glu	Thr	Leu	Asp	Asp	Ala	Glu	Ser	Asp
			565						570					575
Ala	Val	Leu	Gly	Thr	Glu	Asp	Ala	Gly	Asp	Ala	Asp	Arg	Phe	Leu
			580					585					590	
Ala	Leu	Ala	Asp	His	Thr	Arg	Ala	Val	Asp	Trp	Glu	Ala	Val	Leu
	595						600				605			
Arg	Ala	Gly	Leu	Val	Asp	Gly	Gln	Gly	Lys	Phe	Leu	Leu	Pro	Asp
	610					615					620			
Thr	Thr	Pro	Arg	Glu	Leu	Asp	Gly	Trp	Phe	Arg	Val	Asp	Thr	Glu
625					630					635				640
Pro	Arg	Ser	Glu	Pro	Ala	Ala	Leu	Arg	Gly	Arg	Trp	Val	Val	Val
				645					650					655
Glu	Gly	His	Glu	Glu	Asp	Gly	Trp	Thr	Val	Glu	Val	Arg	Ser	Ala
			660				665						670	
Ala	Glu	Ala	Ala	Glu	Pro	Glu	Val	Thr	Arg	Gly	Val	Gly	Gly	Leu
	675						680					685		
Gly	Asp	Cys	Ala	Gly	Val	Leu	Leu	Ala	Leu	Glu	Gly	Asp	Gly	Ala
	690					695				700				
Gln	Thr	Leu	Val	Val	Arg	Glu	Leu	Asp	Ala	Glu	Gly	Ile	Asp	Ala
705					710					715				720
Leu	Trp	Thr	Val	Phe	Gly	Asp	Ala	Gly	Ser	Pro	Val	Ala	Arg	Pro
				725					730					735
Gln	Ala	Lys	Leu	Trp	Leu	Gly	Gln	Val	Ala	Ser	Leu	Arg	Gly	Pro
			740				745						750	
Trp	Thr	Gly	Leu	Val	Leu	Pro	His	Met	Pro	Asp	Pro	Glu	Leu	Arg
	755						760					765		
Arg	Leu	Thr	Val	Leu	Ala	Gly	Ser	Glu	Asp	Gln	Val	Val	Ala	Asp
	770					775					780			
Val	Arg	Ala	Arg	Leu	Ser	Pro	Ala	His	Val	Thr	Ala	Thr	Ser	Glu
785					790					795				800
Ala	Val	Gly	Ile	Val	Gly	Thr	Ala	Gly	Leu	Ala	Glu	Val	Ala	Trp
				805					810					815
Gly	Arg	Ala	Glu	His	Ala	Val	Ser	Arg	Arg	Gly	Pro	Asp	Thr	Glu
			820					825					830	
Val	Gly	Asp	Thr	Ala	Glu	Leu	Thr	Asp	Leu	Ala	Arg	Val	Ser	Val
	835						840					845		
Cys	Val	Ser	Ser	Arg	Glu	Pro	Val	Arg	Glu	Ile	Val	His	Gly	Leu
	850					855					860			
Glu	Gln	Gly	Asp	Val	Val	Arg	Gly	Val	Val	Ala	Ala	Gly	Leu	Pro
865					870					875				880
Gln	Val	Ala	Ile	Asn	Asp	Met	Asp	Glu	Ala	Ala	Phe	Asp	Glu	Val

Ala	Arg	Arg	Gln	Leu	Glu	Ser	Cys	Leu	Glu	Pro	Gly	Val	Asp	Ala	Ala	
			180					185					190			
Ile	Ala	Asn	Leu	Asp	Thr	Arg	Asp	Asp	Ala	Asp	Arg	Leu	Trp	Leu	Ser	
		195					200					205				
Ile	Thr	Val	Thr	Leu	Val	Val	Ala	Leu	Arg	Asn	Glu	Leu	Ala	Thr	His	
	210					215					220					
Val	Glu	Pro	Thr	Pro	His	Val	Asp	Ser	Ser	Gly	Val	Ala	Leu	Leu	Ala	
225					230					235					240	
Gly	Asn	Gln	Pro	Arg	Arg	Gly	Glu	Arg	Thr	Arg	Ala	Ile	Val	Val	Glu	
				245					250					255		
Ala	Glu	Arg	Glu	His	Arg	Glu	Thr	Thr	Ala	His	Asp	Gly	Arg	Pro	Val	
			260					265					270			
Leu	Val	Val	Ala	Arg	Thr	Thr	Ala	Ala	Leu	Arg	Ala	Gln	Ile	Ala	Glu	
		275					280					285				
Leu	Leu	Glu	Arg	Pro	Asp	Ala	Asp	Leu	Ala	Gly	Val	Gly	Leu	Gly	Leu	
	290					295					300					
Thr	Thr	Ala	Arg	His	Glu	His	Ala	Val	Val	Ala	Ser	Thr	Arg	Glu	Glu	
305					310					315					320	
Ala	Val	Arg	Gly	Arg	Glu	Ile	Ala	Ala	Ala	Thr	Ala	Asp	Ala	Val	Val	
				325					330					335		
Glu	Gly	Val	Thr	Glu	Val	Asp	Gly	Arg	Asn	Val	Val	Phe	Leu	Ser	Ala	
			340				345						350			
Gly	Ala	Glu	Ser	Ser	Ser	Pro	Gly	Lys	Ile	Arg	Ala	Asp	Glu	Ser	Met	
	355						360					365				
Ala	Pro	Met	Gln	Asp	Trp	Lys	Val	Ser	Asp	Val	Leu	Arg	Gln	Ala	Pro	
	370					375					380					
Gly	Ala	Pro	Gly	Leu	Asp	Val	Val	Leu	Val	Met	Val	Glu	Leu	Arg		
385					390				395					400		
Ser	Tyr	Val	Glu	Ala	Val	Gln	Ile	His	Ala	Ala	Leu	Thr	Leu	Glu	Asp	
				405					410					415		
Ala	Ala	Lys	Ile	Val	Val	Gly	Arg	Ser	Arg	Ile	Met	Arg	Ser	Leu	Ser	
			420					425					430			
Gly	Glu	Gly	Gly	Ala	Ala	Val	Ala	Leu	Gly	Glu	Ala	Ala	Val	Arg	Glu	
	435						440					445				
Arg	Leu	Arg	Pro	Trp	Gln	Asp	Arg	Leu	Ser	Val	Ala	Gly	Arg	Ser	Val	
	450					455					460					
Val	Val	Ser	Glu	Pro	Gly	Ala	Leu	Arg	Ala	Phe	Ser	Glu	Asp	Cys	Ala	
465					470				475					480		
Ala	Glu	Gly	Ile	Arg	Val	Arg	Asp	Ile	Asp	Asp	Tyr	Ser	Ser	Pro	Gln	
				485					490					495		
Ile	Glu	Arg	Val	Arg	Glu	Glu	Leu	Leu	Glu	Thr	Thr	Gly	Asp	Ile	Ala	
			500					505					510			
Pro	Arg	Pro	Ala	Arg	Val	Pro	Phe	His	Thr	Val	Glu	Ser	Arg	Ser	Met	
		515					520						525			
Asp	Gly	Thr	Glu	Leu	Asp	Ala	Arg	Tyr	Arg	Asn	Ile	Glu	Thr	Arg	Ala	
	530					535					540					
Asp	Val	Thr	Arg	Leu	Ala	Glu	Ser	Tyr	Asp	Ala	Ile	Val	Pro	Val	Val	
545					550					555				560		
Val	Gln	Ala	Val	Glu	Gln	Val	Glu	Glu	Ala	Asp	Gly	Ala	Glu	Asp		
				565					570					575		
Ala	Val	Val	Val	Gly	Ser	His	Asp	Gly	Gly	Asp	Leu	Ser	Ala	Phe	Leu	
			580					585					590			
Arg	Ser	Met	Ala	Thr	His	Val	Ser	Asp	Ile	Arg	Trp	Asp	Val	Ala	Leu	
		595					600						605			
Pro	Gly	Ala	Ala	Pro	Phe	Ala	Thr	Gln	Arg	Lys	Tyr	Leu	Gln	Pro	Ala	
	610					615					620					
Ala	Pro	Ala	Ala	Ala	Ser	Glu	Leu	Ala	Arg	Val	Ser	Thr	Pro	Ile	Glu	
625					630					635				640		
Lys	Pro	Glu	Ser	Gly	Asn	Leu	Asp	Gly	Asp	Trp	Val	Val	Thr	Pro	Leu	
				645					650					655		
Ile	Ser	Pro	Glu	Trp	Thr	Glu	Met	Leu	Cys	Glu	Ala	Ile	Asn	Ala	Asn	
			660					665					670			

Gly	Arg	Ala	Leu	Arg	Cys	Glu	Val	Asp	Thr	Ser	Ala	Ser	Arg	Thr	Glu	675	680	685
Met	Ala	Gln	Ala	Val	Ala	Gln	Ala	Gly	Thr	Gly	Phe	Arg	Gly	Leu	Leu	690	695	700
Leu	Ser	Ser	Asp	Glu	Ser	Ala	Cys	Arg	Pro	Gly	Val	Pro	Ala	Gly	Ala	705	710	715
Val	Gly	Leu	Leu	Thr	Val	Gln	Ala	Leu	Gly	Asp	Ala	Gly	Val	Asp	Ala	725	730	735
Pro	Val	Trp	Cys	Leu	Gln	Gly	Arg	Thr	Pro	Ala	Asp	Asp	Asp	Leu	Ala	740	745	750
Arg	Pro	Ala	Gln	Thr	Thr	Ala	His	Phe	Ala	Gln	Val	Ala	Gly	Leu	Leu	755	760	765
Pro	Gly	Arg	Trp	Gly	Gly	Val	Val	Leu	Pro	Glu	Ser	Val	Asp	Asp	Ala	770	775	780
Ala	Leu	Arg	Leu	Leu	Val	Val	Leu	Arg	Gly	Gly	Gly	Arg	Ala	Glu	Asp	785	790	795
His	Leu	Val	Asp	Gly	Arg	Leu	His	Gly	Arg	Val	Val	Arg	Ala	Ser	Leu	805	810	815
Pro	Gln	Ser	Gly	Ser	Arg	Ser	Trp	Thr	His	Val	Val	Ala	Ala	Ser	Pro	820	825	830
Val	Asp	Gln	Ile	Val	Trp	Ala	Asp	Arg	Ala	Glu	Arg	Val	Ala	Gly	Ala	835	840	845
Cys	Pro	Gly	Asp	Asp	Leu	Ala	Ala	Val	Glu	Glu	Ala	Ala	Ser	Ala	Val	850	855	860
Val	Cys	Gln	Ala	Ala	Ala	Leu	Arg	Glu	Ala	Leu	Gly	Asp	Glu	Pro	Val	865	870	875
Thr	Ala	Leu	Val	Ala	Gly	Thr	Leu	Thr	Asn	Phe	Gly	Ser	Ile	Ser	Glu	885	890	895
Val	Ala	Pro	Glu	Glu	Phe	Ala	Glu	Thr	Ile	Ala	Ala	Thr	Ala	Leu	Leu	900	905	910
Ala	Val	Asp	Val	Leu	Gly	Asp	Arg	Ala	Val	Glu	Arg	His	Val	Tyr	Cys	915	920	925
Val	Gly	Ile	Trp	Gly	Gly	Ala	Gly	Met	Ala	Ala	Ala	Ala	Gly	Ser	Ala	930	935	940
Tyr	Asp	Ala	Leu	Glu	His	His	Ala	Arg	Arg	Ser	Cys	Thr	Ser	Val	Ala	945	950	955
Thr	Pro	Leu	Pro	Gly	Gly	Ala	Val	Asp	Asp	Gly	Tyr	Leu	Arg	Glu	Arg	965	970	975
Leu	Arg	Ser	Leu	Ser	Ala	Asp	Arg	Met	Arg	Thr	Trp	Glu	Arg	Val	Ala	980	985	990
Ala	Gly	Pro	Val	Ser	Val	Ala	Val	Ala	Asp	Val	Asp	Trp	Pro	Val	Leu	995	1000	1005
Ser	Glu	Gly	Phe	Ala	Thr	Arg	Pro	Thr	Ala	Leu	Phe	Ala	Glu	Leu	Ala	1010	1015	1020
Gly	Arg	Gly	Gly	Gln	Ala	Glu	Ala	Glu	Pro	Asp	Ser	Gly	Pro	Thr	Gly	1025	1030	1035
Glu	Pro	Ala	Gln	Arg	Leu	Gly	Leu	Ser	Pro	Asp	Glu	Gln	Gln	Glu	Asn	1045	1050	1055
Leu	Glu	Leu	Val	Ala	Asn	Ala	Val	Glu	Val	Leu	His	Glu	Ser	Ala	Ala	1060	1065	1070
Glu	Ile	Asn	Val	Arg	Arg	Ala	Ser	Glu	Leu	Leu	Asn	Met	Ala	Lys	Arg	1075	1080	1085
Leu	Ser	Ala	Ser	Thr	Leu	Arg	Leu	Pro	Ala	Ser	Leu	Val	Phe	Asp	Thr	1090	1095	1100
Val	Thr	Ala	Leu	Gln	His	Leu	Arg	Ala	Arg	Val	Gly	Asp	Ala	Asp	Gln	1105	1110	1115
Ala	Ala	Val	Arg	Val	Val	Gly	Ala									1125		

<210> 39
<211> 1224

<212> PRT
 <213> Artificial Sequence

<220>

<223> Alignment of the EryA SU

<400> 39

Ala	Asp	Glu	Ser	Glu	Ile	Ile	Gly	Ile	Gly	Phe	Gly	Ile	Gly	Ser	Glu	1	5	10	15
Gln	Leu	Arg	Val	Leu	Ala	Glu	Gly	Ala	Asn	Leu	Thr	Thr	Gly	Phe	Ala	20	25	30	
Asp	Ile	Gly	Arg	Leu	Tyr	His	Pro	Asp	Pro	Asp	Asn	Pro	Gly	Thr	Ser	35	40	45	
Tyr	Val	Asp	Lys	Gly	Pro	Leu	Thr	Asp	Ala	Asp	Pro	Gly	Ile	Thr	Leu	50	55	60	
Met	Leu	Met	Thr	Ala	Ala	Val	Arg	Ile	Asp	Asp	Ala	Arg	Gly	Thr	Asp	65	70	75	80
Val	Met	Asn	Gly	Gln	Ser	Met	Gln	Leu	Leu	Ala	Gly	Glu	Ala	Glu	Arg	85	90	95	
Val	Asp	Gln	Gly	Ile	Asn	Ser	Ala	Ser	Leu	Ile	Ala	Thr	Phe	Trp	Ala	100	105	110	
Leu	Thr	Ser	Val	Gly	Ile	Ile	Met	Gln	Ala	Arg	Gly	Glu	Cys	Ser	Leu	115	120	125	
Leu	Ala	Val	Thr	Ser	Asp	Tyr	Thr	Phe	Val	Asp	Ser	Thr	Gln	Arg	Gly	130	135	140	
Ala	Ser	Cys	Ala	Ser	Ala	Arg	Asp	Ala	Leu	Ser	Val	Ala	Ala	Leu	Val	145	150	155	160
Glu	Pro	Arg	Ala	Asn	His	Gln	Ala	Val	Leu	Arg	Ser	Val	Gln	Ala	Asn	165	170	175	
Pro	Ser	Glu	Arg	Gln	Leu	Ala	Ala	Ser	Val	Pro	Ala	Ala	Val	Asp	Val	180	185	190	
Glu	Ile	Ala	Gly	Ile	Ala	Thr	Gln	Asp	Asp	Arg	Leu	Arg	Leu	Thr	Ile	195	200	205	
Thr	Ala	Ala	Ile	Val	Val	Ala	Met	Arg	His	Met	Leu	Arg	Ser	His	Ala	210	215	220	
Asp	Leu	Ser	Pro	His	Ile	Asp	Glu	Ser	Ala	Val	Glu	Val	Ile	Arg	Glu	225	230	235	240
Glu	Val	Pro	Pro	Ala	Gly	Glu	Arg	Pro	Gly	Ser	Val	Val	Val	Glu	Ala	245	250	255	
Ala	Glu	Gln	Glu	Ala	Ala	Arg	Thr	Glu	Arg	Gly	Pro	Leu	Phe	Val	Leu	260	265	270	
Gly	Arg	Ser	Glu	Ala	Val	Val	Ala	Arg	Ala	Leu	Ala	Glu	His	Leu	Arg	275	280	285	
Asp	Thr	Pro	Glu	Leu	Gly	Leu	Thr	Asp	Ala	Ala	Trp	Thr	Leu	Thr	Gly	290	295	300	
Ala	Arg	Phe	Asp	Val	Ala	Val	Gly	Asp	Asp	Arg	Ala	Gly	Val	Cys	Ala	305	310	315	320
Glu	Asp	Ala	Leu	Glu	Arg	Pro	Ser	Ala	Asp	Ala	Val	Ala	Pro	Val	Thr	325	330	335	
Ser	Ala	Pro	Arg	Lys	Pro	Val	Leu	Val	Ala	Val	Ala	Arg	Asp	Glu	Ser	340	345	350	
Ser	Glu	Glu	Ser	Met	Ser	Arg	Ala	Glu	Ala	Leu	Ser	Pro	His	Thr	Asp	355	360	365	
Trp	Lys	Leu	Leu	Asp	Val	Val	Arg	Gly	Asp	Gly	Gly	Pro	Asp	Pro	His	370	375	380	
Glu	Asp	Ile	Val	Leu	Ser	Ile	Met	Val	Glu	Leu	Arg	Ala	His	Val	Thr	385	390	395	400
Ala	Val	Gln	Ile	His	Ala	Ala	Leu	Ser	Leu	Glu	Ala	Ala	Ala	Lys	Val	405	410	415	
Val	Ala	Leu	Arg	Ser	Gln	Val	Leu	Arg	Glu	Leu	Asp	Asp	Gln	Gly	Gly	420	425	430	
Val	Ser	Val	Gly	Ala	Ser	Arg	Asp	Glu	Leu	Glu	Thr	Val	Leu	Ala	Arg				

930	Ala	Glu	Ile	Glu	Asp	Ile	Ala	Ser	Ala	Glu	Ile	Ala	Cys	Thr	Ala	Asp
945	Arg	Asp	Ala	Leu	Ser	Ala	Leu	Leu	Asp	Gly	Leu	Pro	Arg	Pro	Leu	Thr
				965						970						975
	Gly	Val	Val	Ala	Ala	Gly	Val	Leu	Ala	Asp	Gly	Leu	Val	Thr	Ser	Ile
				980					985					990		
	Asp	Glu	Pro	Ala	Val	Glu	Gln	Val	Leu	Arg	Ala	Val	Asp	Ala	Ala	Trp
			995					1000					1005			
	Asn	His	Leu	Thr	Ala	Asn	Thr	Gly	Leu	Ser	Phe	His	Val	Leu	Phe	Ala
	1010					1015						1020				
	Ser	Val	Leu	Ala	Gly	Pro	Gly	Gln	Gly	Val	Ala	Ala	Ala	Asn	Glu	Ser
1025						1030					1035				1040	
	Asn	Ala	Leu	Ala	Leu	Arg	Thr	Arg	Leu	Pro	Ala	Lys	Ala	Leu	Gly	Gly
				1045						1050					1055	
	Leu	Gln	Ala	Ser	Glu	Met	Thr	Ser	Gly	Leu	Gly	Asp	Arg	Ile	Ala	Arg
			1060						1065					1070		
	Thr	Val	Ala	Ala	Leu	Pro	Thr	Glu	Arg	Leu	Ala	Leu	Phe	Asp	Ser	Ala
			1075					1080					1085			
	Arg	Arg	Gly	Gly	Glu	Val	Val	Phe	Pro	Leu	Ser	Ile	Asn	Arg	Ser	Ala
1090						1095						1100				
	Leu	Arg	Arg	Glu	Phe	Val	Pro	Glu	Val	Leu	Arg	Gly	Met	Val	Arg	Ala
1105						1110						1115			1120	
	Lys	Leu	Arg	Ala	Ala	Gly	Gln	Ala	Glu	Ala	Ala	Gly	Pro	Asn	Val	Val
				1125						1130					1135	
	Asp	Arg	Leu	Gly	Arg	Ser	Glu	Ser	Asp	Gln	Val	Ala	Gly	Ala	Glu	Leu
			1140						1145					1150		
	Val	Arg	Ser	His	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Ala	Asp	Gln	Leu	Pro
		1155						1160					1165			
	Glu	Arg	Lys	Ala	Lys	Asp	Phe	Leu	Ala	Val	Glu	Asn	Arg	Leu	Gly	Thr
1170						1175						1180				
	Ala	Thr	Val	Arg	Leu	Pro	Ser	Thr	Leu	Val	Phe	Asp	Thr	Pro	Leu	Ala
1185						1190					1195				1200	
	Val	Glu	His	Leu	Arg	Asp	Arg	Phe	Ala	Ala	Ser	Pro	Ala	Val	Asp	Ile
				1205					1210					1215		
	Gly	Asp	Arg	Leu	Asp	Glu	Leu	Glu								
				1220												

<210> 40

<211> 1118

<212> PRT

<213> Artificial Sequence

<220>

<223> Alignment of the EryA SU

<400> 40

His	Arg	Ala	Gly	Glu	Ile	Ile	Gly	Met	Ala	Phe	Asp	Val	Asp	Ser	Glu
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Ser	Phe	Glu	Phe	Val	Ser	Gly	Gly	Gly	Asp	Ala	Ile	Ala	Glu	Ala	Ala
			20				25						30		
Glu	Pro	Asp	Pro	Asp	Ala	Arg	Leu	Gly	Met	Leu	Ala	Ala	Gly	Asp	Ala
		35					40					45			
Gly	Ile	Ser	Leu	Met	Ile	Met	Ile	Ser	Ala	Leu	Arg	His	Asp	Val	Ser
	50					55					60				
Arg	Gly	Ser	Ala	Ile	Val	Gly	Thr	Val	Asp	Gly	Pro	Arg	Pro	Asp	Glu
65					70					75					80
Ala	Pro	Asp	Glu	Val	Leu	Val	Gly	Thr	Thr	Ala	Ser	Ser	Ala	Val	Ala
				85					90					95	
Cys	Leu	Leu	Ala	Met	Thr	Gly	Thr	Ala	Leu	Ile	Met	Glu	Ser	Arg	Asp
			100					105						110	

Glu	Cys	Gly	Leu	Ile	Ala	Val	Thr	Ser	Ser	Gly	Ala	Phe	Glu	Arg
		115					120					125		
Ser	Gln	Gly	Gly	Ala	Ala	Cys	Pro	Ser	Lys	Ala	Asp	Gly	Leu	Ala
		130				135					140			
Gly	Val	Leu	Val	Gln	Arg	Ala	Arg	Glu	Arg	Pro	Ala	Val	Leu	Arg
145					150					155				160
Val	Gln	Thr	Ser	Pro	Ala	Gln	Arg	Arg	Leu	Glu	Asn	Ala	Val	Arg
				165					170					175
Gly	Val	Asp	Tyr	Arg	Ile	Val	His	Leu	Ser	Thr	Ala	Glu	Asp	Pro
		180						185					190	Asp
Asp	Leu	Trp	Ile	Ser	Ile	Thr	Val	Ala	Met	Ala	Val	Ala	Leu	Arg
		195					200					205		His
Glu	Met	Arg	Thr	His	Phe	Asp	Pro	Ser	Pro	Gln	Ile	Glu	Asp	Leu
	210					215					220			Ala
Val	Ser	Val	Val	Ser	Gln	Ala	Arg	Ser	Pro	Ala	Gly	Glu	Arg	Pro
225					230					235				240
Ser	Ile	Val	Val	Glu	Ala	Glu	Ala	Asp	Glu	Pro	Glu	Pro	Ala	Pro
				245					250					255
Ser	Gly	Pro	Val	Leu	Val	Leu	Gly	Arg	Asp	Glu	Gln	Ala	Met	Arg
		260						265					270	Gly
Arg	Leu	Ala	Asp	His	Leu	Ala	Arg	Glu	Pro	Arg	Asn	Ser	Leu	Arg
		275					280					285		Asp
Thr	Gly	Phe	Thr	Leu	Thr	Arg	Ser	Ala	Trp	Glu	His	Val	Val	Val
	290					295					300			Gly
Asp	Arg	Asp	Asp	Ala	Leu	Ala	Gly	Arg	Ala	Val	Asp	Arg	Ile	Ala
305					310					315				320
Arg	Thr	Ala	Thr	Gly	Gln	Ala	Arg	Thr	Arg	Arg	Gly	Val	Ala	Met
			325						330					335
Ala	Gln	Ala	Arg	Asp	Arg	Glu	Ser	Gln	Asp	Ser	Ile	Arg	Asp	Glu
		340						345					350	Arg
Ala	Leu	Ala	Pro	His	Val	Asp	Trp	Ser	Leu	Thr	Asp	Leu	Leu	Ser
		355					360					365		Gly
Ala	Arg	Pro	Leu	Asp	Asp	Val	Ala	Leu	Ala	Val	Met	Val	Ala	Leu
	370					375					380			Arg
Ser	His	Val	Glu	Ala	Val	Gln	Ile	His	Ala	Ala	Leu	Thr	Leu	Glu
385					390					395				400
Ala	Ala	Lys	Leu	Val	Ala	Val	Arg	Ser	Arg	Val	Leu	Ala	Arg	Leu
			405						410					415
Gly	Gln	Gly	Gly	Ala	Ser	Phe	Gly	Leu	Gly	Thr	Glu	Gln	Ala	Ala
		420						425					430	Glu
Arg	Ile	Gly	Arg	Phe	Ala	Gly	Ala	Leu	Ser	Ile	Ser	Gly	Arg	Ser
	435						440					445		Val
Val	Val	Ala	Glu	Ser	Gly	Pro	Leu	Asp	Glu	Leu	Ile	Ala	Glu	Cys
	450					455					460			Glu
Ala	Glu	Gly	Ile	Thr	Ala	Arg	Arg	Ile	Pro	Asp	Tyr	Ser	Ser	Pro
465					470					475				480
Val	Glu	Ser	Ile	Arg	Glu	Glu	Leu	Leu	Thr	Glu	Leu	Ala	Gly	Ile
			485						490					495
Pro	Val	Ser	Ala	Asp	Val	Ala	Leu	Tyr	Thr	Thr	Thr	Gly	Gln	Pro
			500					505					510	Ile
Asp	Thr	Ala	Thr	Met	Asp	Thr	Ala	Tyr	Ala	Asn	Leu	Glu	Gln	Arg
		515					520					525		Gln
Asp	Thr	Arg	Gln	Leu	Ala	Glu	Ala	Phe	Asp	Ala	Val	Val	Pro	Val
	530					535					540			Leu
Thr	Val	Gly	Ile	Glu	Ala	Thr	Leu	Asp	Ser	Ala	Leu	Pro	Ala	Asp
545					550					555				560
Gly	Ala	Cys	Val	Val	Gly	Thr	Arg	Asp	Arg	Gly	Gly	Leu	Ala	Asp
			565						570					575
His	Thr	Ala	Leu	Gly	Glu	Tyr	Ala	Gln	Glu	Val	Asp	Trp	Ser	Pro
			580					585					590	Ala
Phe	Ala	Asp	Ala	Arg	Pro	Val	Glu	Val	Gln	Arg	Gln	Tyr	Leu	Pro
		595					600						605	Ile

Pro Thr Gly Gly Arg Ala Arg Glu Asp Asp Asp Trp Arg G Val Val
 610 615 620
 Arg Glu Ala Glu Trp Glu Ser Ala Ser Leu Ala Gly Arg Val Leu Val
 625 630 635 640
 Thr Gly Pro Gly Val Pro Ser Glu Leu Ser Asp Ala Ile Arg Ser Gly
 645 650 655
 Leu Glu Gln Ser Ala Thr Val Leu Thr Cys Asp Val Glu Ser Arg Ser
 660 665 670
 Thr Ile Gly Thr Ala Leu Glu Ala Ala Asp Thr Asp Ala Leu Ser Thr
 675 680 685
 Val Leu Leu Ser Arg Asp Gly Glu Ala Val Asp Pro Ser Leu Asp Ala
 690 695 700
 Leu Ala Val Gln Ala Leu Gly Ala Ala Gly Val Glu Ala Pro Leu Trp
 705 710 715 720
 Val Leu Arg Asn Gln Val Ala Asp Gly Glu Leu Val Asp Pro Ala Gln
 725 730 735
 Ala Met Val Gly Leu Gly Arg Val Val Gly Ile Gln Pro Gly Arg Trp
 740 745 750
 Gly Gly Leu Val Leu Val Asp Ala Asp Ala Ala Ser Ile Arg Ser Leu
 755 760 765
 Ala Val Leu Ala Asp Pro Arg Gly Glu Glu Gln Val Ile Ala Asp Gly
 770 775 780
 Ile Lys Val Ala Leu Val Pro Ala Pro Ala Arg Ala Ala Arg Thr Arg
 785 790 795 800
 Trp Ser Arg Val Val Gly Thr Gly Gly Ile Ala His Val Ala Trp Ala
 805 810 815
 Arg Ser Ala Glu His Val Leu Gly Arg Arg Gly Ala Asp Ala Pro Gly
 820 825 830
 Ala Ser Glu Arg Glu Glu Leu Thr Ala Leu Thr Gly Val Thr Ile Ala
 835 840 845
 Cys Val Ala Asp Arg Ala Arg Leu Glu Ala Val Leu Ala Ala Glu Arg
 850 855 860
 Ala Glu Gly Arg Thr Val Ser Ala Val Met Ala Ala Gly Val Ser Thr
 865 870 875 880
 Ser Thr Pro Leu Asp Asp Leu Thr Glu Ala Glu Phe Thr Glu Ile Ala
 885 890 895
 Asp Val Val Arg Gly Thr Val Asn Asp Leu Cys Pro Asp Leu Asp Ala
 900 905 910
 His Val Leu Phe Asn Gly Val Trp Gly Ser Pro Gly Leu Ala Ser Ala
 915 920 925
 Ala Ala Asn Ala Phe Asp Gly Phe Arg Arg Arg Ser Glu Ala Pro Val
 930 935 940
 Thr Ser Ile Ala Gly Leu Gly Gln Asn Met Ala Gly Asp Glu Gly Gly
 945 950 955 960
 Glu Tyr Leu Arg Ser Gln Leu Arg Ala Met Asp Pro Asp Arg Val Glu
 965 970 975
 Glu Leu His Ile Thr Asp His Gly Gln Thr Ser Val Ser Val Val Asp
 980 985 990
 Met Asp Arg Arg Arg Phe Val Glu Leu Phe Thr Ala Arg His Arg Pro
 995 1000 1005
 Leu Phe Asp Glu Ile Ala Gly Ala Arg Ala Glu Ala Arg Gln Ser Glu
 1010 1015 1020
 Glu Gly Pro Ala Leu Ala Gln Arg Leu Ala Leu Ser Thr Ala Glu Arg
 1025 1030 1035 1040
 Arg Glu His Ala His Leu Ile Arg Ala Glu Val Ala Val Leu His Gly
 1045 1050 1055
 Asp Asp Ala Ala Ile Asp Arg Asp Arg Ala Arg Asp Phe Met Thr Val
 1060 1065 1070
 Asp Asn Arg Leu Ala Ala Val Thr Val Arg Glu Ala Ala Thr Val Val
 1075 1080 1085
 Phe Asp Thr Ile Thr Arg Leu Asp His Tyr Leu Glu Arg Val Gly Ala
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Ala Glu Ala Glu Gln Ala Pro Ala Leu Val Arg Glu Val P
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 <211> 1099
 <212> PRT
 <213> Artificial Sequence

<220>
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 Glu Leu Glu Phe Ile Val Gly Arg Gly Asp Ala Val Thr Glu Met Thr
 20 25 30
 Asp Leu Asp Ala Leu Phe Asp Pro Asp Pro Gln Arg His Gly Thr Ser
 35 40 45
 Tyr Ser Arg His Ala Phe Leu Asp Gly Ala Asp Ala Ala Ile Ser Leu
 50 55 60
 Met Gln Val Thr Thr Leu Phe Asn Ile Asp His Ser Arg Gly Ser Asp
 65 70 75 80
 Leu Ala Ala Tyr Gln Gly Gly Gln Asp Ala Val Val Pro Glu Asp Ser
 85 90 95
 Glu Leu Leu Thr Asn Ser Ser Ala Val Val Ala Val Leu Leu Ala Val
 100 105 110
 Thr Ser Val Ala Leu Ser Cys Gly Ser Asp Gly Asp Cys Gly Leu Val
 115 120 125
 Ala Val Ser Ala Gly Glu Val Phe Thr Glu Ser Arg Gln Gly Gly Ala
 130 135 140
 Val Cys Ala Ser Ala Glu Asp Gly Phe Ala Val Ala Val Val Leu Gln
 145 150 155 160
 Arg Asp Arg Ala Arg Gln Gly Val Val Ala Ser Leu Gln Ala Ser Val
 165 170 175
 Ala Gln Arg Lys Trp Ala Arg Ala Ile Thr Gly Ala Val Ala Val Arg
 180 185 190
 Val Ala Ser Leu Ala Thr Lys Ser Gly Ser Ser Gly Val Leu Leu Ser
 195 200 205
 Ile Ala Val Ala Ile Val Val Gly Leu Asn Arg Leu Val Pro Met Cys
 210 215 220
 Arg Gly Arg Ser Pro Leu Ile Glu Ser Ser Gly Val Glu Leu Ala Glu
 225 230 235 240
 Ala Val Ser Pro Pro Pro Ala Ala Asp Gly Val Gly Ala Val Val Ile
 245 250 255
 Ala Pro Glu Pro Glu Pro Leu Pro Glu Pro Gly Pro Val Gly Val Leu
 260 265 270
 Ala Ala Ala Asn Ser Val Val Leu Leu Ala Arg Thr Glu Thr Ala Leu
 275 280 285
 Ala Arg Leu Leu Glu Ser Ala Val Asp Asp Ser Val Pro Leu Thr Ala
 290 295 300
 Leu Ala Ser Ala Leu Thr Gly Ala His Leu Pro Arg Ala Leu Ile Ala
 305 310 315 320
 Gly Asp His Glu Gln Leu Arg Gly Gln Arg Ala Val Glu Val Ala Ala
 325 330 335
 Pro Gly Ala Thr Thr Gly Thr Ala Ser Ala Gly Gly Val Val Phe Val
 340 345 350
 Ala Glu Ala Arg Gly Ser Val Pro Glu Ser Ile Ala Glu Asp Ala Val
 355 360 365
 Leu Ser Glu Val Ala Gly Phe Ser Ala Ser Glu Val Leu Glu Gln Arg
 370 375 380
 Pro Asp Ala Pro Ser Leu Glu Asp Val Val Leu Ser Val Met Val Arg

385	Leu	Gly	Ala	Cys	Val	Ser	Ser	Ile	Gln	Ile	Val	Ala	Val	Leu	Ser	Leu
					405					410					415	
	Glu	Asp	Gly	Val	Arg	Val	Val	Ala	Leu	Arg	Ala	Lys	Ala	Leu	Arg	Ala
				420					425					430		
	Leu	Ala	Gly	Arg	Gly	Gly	Val	Ser	Leu	Ala	Ala	Pro	Gly	Glu	Arg	Ala
			435					440					445			
	Arg	Ala	Leu	Ile	Ala	Pro	Trp	Glu	Asp	Arg	Ile	Ser	Val	Ala	Ser	Ser
			450				455					460				
	Ser	Val	Val	Val	Ser	Asp	Pro	Glu	Ala	Leu	Ala	Glu	Leu	Val	Ala	Arg
465						470					475					480
	Cys	Glu	Asp	Glu	Gly	Val	Arg	Ala	Lys	Thr	Leu	Pro	Asp	Tyr	Ser	Ser
				485						490					495	
	Arg	His	Val	Glu	Ile	Arg	Glu	Thr	Ile	Leu	Ala	Asp	Leu	Asp	Gly	
			500					505					510			
	Ile	Ser	Ala	Arg	Arg	Ala	Ala	Ile	Pro	Leu	Tyr	Thr	Leu	His	Gly	Glu
			515					520					525			
	Arg	Arg	Asp	Gly	Ala	Asp	Met	Gly	Pro	Arg	Tyr	Asp	Asn	Leu	Ser	Gln
			530				535					540				
	Arg	Asp	Glu	Val	Ser	Ala	Ala	Val	Ala	Asp	His	Ala	Thr	Val	Met	Pro
545						550					555					560
	Val	Ile	Thr	Ala	Ala	Val	Gln	Glu	Ile	Ala	Ala	Asp	Ala	Val	Ala	Ile
				565						570					575	
	Gly	Ser	His	Asp	Thr	Ala	Glu	Glu	His	Ile	Ile	Ala	Glu	Leu	Ala	Arg
			580						585				590			
	His	Val	His	Ala	Val	Asp	Trp	Arg	Asx	Val	Phe	Pro	Ala	Ala	Pro	Pro
			595				600					605				
	Val	Ala	Asn	Glu	Pro	Gln	Tyr	Leu	Ala	Pro	Glu	Val	Ser	Gln	Leu	Ala
			610				615					620				
	Asp	Ser	Arg	Arg	Val	Asp	Arg	Pro	Leu	Ala	Thr	Thr	Pro	Val	Asp	Leu
625						630					635					640
	Glu	Gly	Gly	Phe	Val	His	Gly	Ser	Ala	Pro	Glu	Ser	Leu	Thr	Ser	Ala
				645						650					655	
	Val	Glu	Lys	Ala	Gly	Arg	Val	Val	Pro	Val	Ala	Ser	Ala	Asp	Arg	Glu
			660						665				670			
	Ala	Ser	Ala	Ala	Leu	Arg	Glu	Val	Pro	Gly	Glu	Val	Ala	Gly	Leu	Val
			675					680					685			
	His	Thr	Gly	Ala	Ala	Thr	His	Leu	Ala	His	Gln	Ser	Leu	Gly	Glu	Ala
			690				695					700				
	Gly	Val	Arg	Ala	Pro	Leu	Trp	Leu	Val	Ser	Arg	Ala	Leu	Gly	Glu	Ser
705						710					715					720
	Glu	Pro	Val	Asp	Pro	Glu	Gln	Ala	Met	Val	Trp	Leu	Gly	Arg	Val	Met
				725						730					735	
	Gly	Leu	Thr	Pro	Glu	Arg	Trp	Gly	Gly	Leu	Val	Leu	Pro	Ala	Glu	Pro
			740						745					750		
	Ala	Pro	Gly	Asp	Gly	Glu	Ala	Phe	Val	Cys	Leu	Gly	Ala	Asp	Gly	His
			755					760					765			
	Glu	Asp	Gln	Val	Ile	Asp	His	Ala	Arg	Tyr	Gly	Arg	Leu	Val	Arg	Ala
			770				775					780				
	Pro	Leu	Gly	Thr	Arg	Glu	Ser	Ser	Trp	Glu	Ala	Ala	Val	Gly	Thr	Gly
785						790					795					800
	Ala	Leu	Gly	His	Val	Ala	His	Ala	Arg	Cys	Val	Glu	Asp	Val	Val	Ser
				805						810					815	
	Arg	Arg	Gly	Val	Asp	Ala	Pro	Gly	Ala	Ala	Glu	Glu	Ala	Glu	Leu	Val
			820						825					830		
	Ala	Ile	Ala	Lys	Thr	Thr	Ile	Thr	Cys	Val	Ala	Asp	Arg	Glu	Gln	Leu
			835					840					845			
	Ser	Lys	Leu	Leu	Glu	Glu	Leu	Arg	Gly	Gln	Gly	Arg	Pro	Val	Arg	Thr
			850				855					860				
	Val	Val	Thr	Ala	Gly	Val	Pro	Glu	Ser	Arg	Pro	Leu	His	Glu	Ile	Gly
865						870				875						880
	Glu	Leu	Glu	Ser	Val	Cys	Ala	Ala	Val	Thr	Gly	Ala	Arg	Leu	Asp	Leu

				885					890					895					
Cys	Pro	Asp	Ala	Glu	Thr	His	Val	Leu	Phe	Gly	Gly	Val	Trp	Gly	Ser				
			900					905					910						
Ala	Asn	Leu	Gly	Ala	Ser	Ala	Ala	Asn	Ala	Tyr	Asp	Ala	Leu	His	Arg				
		915					920					925							
Arg	Ala	Glu	Arg	Ala	Ala	Thr	Ser	Val	Ala	Gly	Ala	Gly	Glu	Gly	Met				
		930				935					940								
Ala	Thr	Gly	Asp	Leu	Glu	Gly	Leu	Thr	Arg	Arg	Leu	Arg	Pro	Met	Ala				
945					950				955						960				
Pro	Glu	Arg	Ile	Arg	Ala	Leu	His	Gln	Ala	Asp	Asn	Gly	Asp	Thr	Cys				
			965					970						975					
Val	Ser	Ile	Ala	Asp	Val	Asp	Trp	Glu	Ala	Phe	Ala	Val	Gly	Phe	Thr				
		980					985					990							
Ala	Arg	Pro	Arg	Pro	Leu	Leu	Asp	Glu	Leu	Val	Thr	Pro	Ala	Val	Gly				
		995					1000					1005							
Ala	Val	Pro	Ala	Val	Gln	Ala	Pro	Ala	Arg	Glu	Met	Thr	Ser	Gln	Glu				
		1010				1015					1020								
Leu	Glu	Phe	Thr	His	Ser	His	Val	Ala	Ile	Leu	His	Ser	Ser	Pro	Asp				
1025					1030				1035					1040					
Ala	Val	Gly	Gln	Asp	Gln	Pro	Thr	Glu	Phe	Leu	Thr	Val	Gly	Asn	Gln				
			1045					1050					1055						
Leu	Gln	Gln	Ala	Thr	Leu	Ala	Leu	Pro	Ala	Thr	Leu	Val	Phe	Glu	Thr				
		1060					1065					1070							
Val	Arg	Arg	Leu	Asp	His	Ile	Gly	Gln	Gln	Asp	Ser	Gly	Thr	Pro	Ala				
		1075				1080						1085							
Arg	Glu	Ala	Ser	Ser	Ala	Leu	Arg	Asp	Gly	Tyr									
		1090				1095													